WHAT IS CLAIMED IS:

1. A method of sequence determination for nucleic acid performing matrix transformation on a waveform signal obtained from a detection part for each fluorochrome by fluorochrome terminator labeling employing a plurality of fluorochromes having different fluorescent waveforms for obtaining a signal waveform every base, and determining a base sequence on the basis thereof, wherein the method obtains a matrix value for performing the matrix transformation from actual sample migration through steps of:

① extracting peaks from a proper range;

② eliminating peaks having irregular peak intervals;

③ classifying the peaks into four groups corresponding to the types of bases;

④ obtaining signal strength ratios of classified the four groups;

⑤ allocating the corresponding bases to the classified four groups; and

⑥ obtaining the matrix value by signal strength ratios of peak waveforms of the respective base groups.

2. The method of sequence determination according to claim 1, wherein

the proper range in the step ① is a certain range of starting points of signals.

3. The method of sequence determination according to claim 1, wherein

the peaks extracted in the step ① are such peaks that the strength of the maximum fluorochrome signal is larger than the minimum standard for peak detection in a used sequence determination program.

4.   The method of sequence determination according to claim 1, wherein

such peaks that signal strengths of fluorochromes of separate waveforms are larger than signal strengths of fluorochromes of adjacent waveforms are eliminated in the step ①.

5.   The method of sequence determination according to claim 1, wherein

the four groups classified in the step ③ are upper four groups having large peak numbers.

6.   The method of sequence determination according to claim 1, wherein

the signal strength ratios in the step ④ are either mean values or central values.

7.   The method of sequence determination according to claim 6, wherein

the signal strength ratios are central values.

8.   The method of sequence determination according to claim 1, wherein

the bases are allocated in the step ⑤ by, when the types of maximum detection signals of four groups are different each other, allocating the types of these maximum detection signals as the base species of respective the groups.

9.   The method of sequence determination according to claim 1, wherein

the bases are allocated in the step ⑤ on the basis of, when the

types of maximum detection signals of two groups are identical to each other, the types of the third largest detection signals of the groups.

10.   The method of sequence determination according to claim 1,

5   wherein

the base sequence is determined with obtained the matrix value for thereafter obtaining a matrix value again with peak signals of the determined base sequence.

10   11.   The method of sequence determination according to claim 1, wherein

conditions are limited thereby simplifying treatment in at least one of the steps ① to ⑥.